Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS

1. *(previously presented):* A method for determining the presence or absence of at least one target sequence (2) in a nucleic acid sample, comprising the steps of:

a) providing to a nucleic acid sample a pair of a first oligonucleotide probe and a second oligonucleotide probe for each target sequence to be detected in the sample, whereby the first oligonucleotide probe has a section (4) at its 5'-end that is complementary to a first part (5) of a target sequence and the second oligonucleotide probe has a section (6) at its 3'-end that is complementary to a second part (7) of the target sequence,

wherein the first (5) and second part (7) of the target sequence are located adjacent to each other, and

wherein the first and second oligonucleotide probes (4, 6) each comprise a tag sequence (8, 9), which tag sequences

(i) are essentially non-complementary to the target sequence ,

(ii) comprise primer-binding sites (12, 13), and

wherein at least one of the tags further comprises a stuffer (11) and a restriction site (10) for a restriction enzyme,

(A) which restriction site (10) is located between the primer-binding site and the section of the oligonucleotide probe (4, 6) that is complementary to the first (5) or second part (7) of the target sequence and

(B) which stuffer (11) is located between the restriction site (10) and the primer-binding site;

b) allowing the oligonucleotide probes to anneal to the adjacent parts of target sequence so that the complementary sections (4,6) of the first and the second oligonucleotide probes are adjacent;

c) providing means (14) for connecting the first and the second oligonucleotide probes annealed adjacently to the target sequence and allowing the complementary sections (4, 6) of the adjacently annealed first and second oligonucleotide probes to become connected, to produce a connected probe (15) corresponding to a target sequence in the sample;

d) amplifying the connected probes from a primer pair (16, 17) to produce an amplified sample (19) comprising amplified connected probes (20);

e) digesting the amplified connected probes with the restriction enzyme to produce a detectable fragment (21);

f) detecting the presence or absence of the target sequence by detecting the presence or absence of the detectable fragment by a detection method based upon molecular mass.

2. *(**currently** amended):* A method according to claim 1 [[2]], wherein the mass of a detectable fragment corresponding to [[a]] one target sequence in a sample differs from the mass of a detectable fragment corresponding to a different target sequence in the sample.

3. *(previously presented):* A method according to claim 2, wherein the detectable fragment is denatured to provide a top single strand and a bottom single strand.

4. *(previously presented):* A method according to claim 3, wherein the top strand comprises the stuffer and wherein the bottom strand is essentially complementary to the top strand.

5. *(previously presented):* A method according to claim 3, wherein the mass of a top strand corresponding to one target sequence in a sample differs from the mass of ~~from~~ the top strand corresponding to a different target sequence in the sample.

6. *(previously presented):* A method according to claim 3, wherein the mass of a bottom strand corresponding to one target sequence in a sample differs from the mass of the bottom strand corresponding to a different target sequence in the sample.

7. *(previously presented):* A method according to claim 3, wherein the difference in mass is due to the mass of the stuffer in the top strand.

8. *(previously presented):* A method according to claim 3, wherein the top strands and/or the bottom strands corresponding to different target sequences in the sample differ in mass by more than 1 Dalton.

9. *(previously presented):* A method according to claim 1, wherein a primer capable of annealing to the primer-binding site in the detectable fragment comprises an affinity label.

10. *(previously presented):* A method according to claim 9, wherein the top strands and/or the bottom strands comprise the affinity label.

11. *(previously presented):* A method according to claim 9, wherein the detectable fragment, the top strand or the bottom strand is purified or isolated or separated from the sample comprising the amplified connected probes using the affinity label.

12. *(previously presented):* A method according to claim 9, wherein the affinity label is biotin.

13. *(previously presented):* A method according to claim 1, wherein the detection method is a mass spectroscopic method.

14. *(previously presented):* A method according to claim 1, wherein the restriction enzyme is a restriction endonuclease.

15. *(previously presented):* A method according to claim 14, wherein the restriction endonuclease is a rare cutter.

16. *(previously presented):* A method according to claim 3, wherein a further difference in mass between top strands corresponding to different target sequences is created by incorporating different primer-binding sites in the oligonucleotide probes to which the different primers can anneal.

17. *(previously presented):* A method according to claim 1, wherein the tag of the oligonucleotide probes comprise said stuffer sequence with a mass from 0 to 20,000 daltons.

18. *(previously presented):* A method according to claim 1, wherein the presence or absence of at least 10different target nucleotide sequences is determined in a nucleic acid sample.

19. *(previously presented):* A method according to claim 1, wherein the length of the complementary section of the oligonucleotide probes is between 15 and 50 nucleotides.

20. *(previously presented):* A method according to claim 1, wherein the length of the primer-binding site is between 12 and 40 nucleotides.

21. *(previously presented):* A method according to claim 1, wherein the length of the tag is between 15 and 540 nucleotides.

22. *(previously presented):* A method according to claim 1, wherein the target nucleotide sequence contains a polymorphism.

23. *(previously presented):* A method according to claim 1, wherein the target nucleotide sequence is cDNA, genomic DNA, a restriction fragment, an adapter-ligated restriction fragment, amplified adapter-ligated restriction fragments or AFLP fragments.

24. *(previously presented):* A method according to claim 1, further comprising a step for removing non-ligated probes.

25. *(previously presented):* A method according to claim 1, wherein at least one of the primers is a selective primer.

26. *(previously presented):* A method according to claim 25, wherein the selective primer comprises

(i) a section that is complementary to at least part of the primer-binding site, and

(ii) a selective section of one to 10 selective nucleotides located immediately adjacent, to the 3' end of the section of (i).

27. *(previously presented):* A method according to claim 26 wherein the section of (i) is complementary to 5 or more nucleotides that form a part of the primer-binding site that is located immediately adjacent to the nucleotides complementary to the selective section of the primer.

28-39: CANCELED